

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/550,498  
Source: PS/10  
Date Processed by STIC: 10/5/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

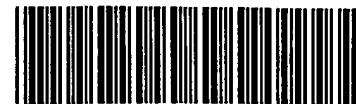
1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

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## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>10/550,498</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ___ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ___ Invalid Line Length	The rules require that a line <b>not exceed</b> 72 characters in length. This includes white spaces.	
3 ___ Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do <b>not</b> use tab codes between numbers; use <b>space characters</b> , instead.	
4 ___ Non-ASCII	The submitted file was <b>not</b> saved in ASCII(DOS) text, as <b>required</b> by the Sequence Rules. <b>Please ensure your subsequent submission is saved in ASCII text.</b>	
5 ___ Variable Length	Sequence(s) ___ contain n's or Xaa's representing more than one residue. <b>Per Sequence Rules, each n or Xaa can only represent a single residue.</b> Please present the <b>maximum</b> number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ___ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>	
7 ___ Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for <b>each</b> skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to <b>include</b> the skipped sequences.	
8 ___ Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If <b>intentional</b> , please insert the following lines for <b>each</b> skipped sequence. <210> sequence id number <400> sequence id number 000	
9 ___ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is <b>MANDATORY</b> if n's or Xaa's are present. In <220> to <223> section, please explain location of <b>n</b> or <b>Xaa</b> , and which residue <b>n</b> or <b>Xaa</b> represents.	
10 ___ Invalid <213> Response	Per 1.823 of Sequence Rules, the only <b>valid</b> <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is <b>required</b> when <213> response is Unknown or is Artificial Sequence	
11 ___ Use of <220>	Sequence(s) <u>1-42</u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is <b>MANDATORY</b> if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 ___ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ___ Misuse of n/Xaa	"n" can <b>only</b> represent a single <u>nucleotide</u> ; "Xaa" can <b>only</b> represent a single <u>amino acid</u>	



PCT

## RAW SEQUENCE LISTING

DATE: 10/05/2005

PATENT APPLICATION: US/10/550,498

TIME: 16:19:28

Input Set : A:\persico.ST25.txt

Output Set: N:\CRF4\10052005\J550498.raw

3 <110> APPLICANT: Minchiotti, Gabriella  
 4 Persico, Maria  
 5 Parisi, Silvia  
 7 <120> TITLE OF INVENTION: METHOD FOR PROMOTING DIFFERENTIATION OF STAMINAL CELL  
 9 <130> FILE REFERENCE: 30242 PCT  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/550,498  
 C--> 12 <141> CURRENT FILING DATE: 2005-09-20  
 14 <160> NUMBER OF SEQ ID NOS: 42  
 16 <170> SOFTWARE: PatentIn version 3.1  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 22  
 20 <212> TYPE: DNA  
 21 <213> ORGANISM: Artificial  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: primer\_bind  
 25 <222> LOCATION: (1)..(22)  
 26 <223> OTHER INFORMATION:  
 W--> 29 <400> 1  
 30 ttccttctca ggtcacgttt gc  
 33 <210> SEQ ID NO: 2  
 34 <211> LENGTH: 21  
 35 <212> TYPE: DNA  
 36 <213> ORGANISM: Artificial  
 38 <220> FEATURE:  
 39 <221> NAME/KEY: primer\_bind  
 40 <222> LOCATION: (1)..(21)  
 41 <223> OTHER INFORMATION:  
 W--> 44 <400> 2  
 45 ggtggggttg gtatcgtttc a  
 48 <210> SEQ ID NO: 3  
 49 <211> LENGTH: 25  
 50 <212> TYPE: DNA  
 51 <213> ORGANISM: Artificial  
 53 <220> FEATURE:  
 54 <221> NAME/KEY: primer\_bind  
 55 <222> LOCATION: (1)..(25)  
 56 <223> OTHER INFORMATION:  
 W--> 59 <400> 3  
 60 aaggatccag gctctgctgt gtgcc  
 63 <210> SEQ ID NO: 4  
 64 <211> LENGTH: 26  
 65 <212> TYPE: DNA  
 66 <213> ORGANISM: Artificial

pg 1-5

Does Not Comply  
Corrected Diskette Needed

This needs explanation on <2237 line> (see item 11 on Err summary sheet)  
 ← not an explanation

← same error

same

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/550,498

DATE: 10/05/2005

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Input Set : A:\persico.ST25.txt

Output Set: N:\CRF4\10052005\J550498.raw

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68 <220> FEATURE:
69 <221> NAME/KEY: primer_bind
70 <222> LOCATION: (1)..(26)
71 <223> OTHER INFORMATION: same
W--> 74 <400> 4
75 acggatccat gtccaacctc tggcgg 26
78 <210> SEQ ID NO: 5
79 <211> LENGTH: 20
80 <212> TYPE: DNA
81 <213> ORGANISM: Artificial
83 <220> FEATURE:
84 <221> NAME/KEY: primer_bind
85 <222> LOCATION: (1)..(20)
86 <223> OTHER INFORMATION: same
W--> 89 <400> 5
90 atgtgccgtg gtgtcgtggt 20
93 <210> SEQ ID NO: 6
94 <211> LENGTH: 20
95 <212> TYPE: DNA
96 <213> ORGANISM: Artificial
98 <220> FEATURE:
99 <221> NAME/KEY: primer_bind
100 <222> LOCATION: (1)..(20)
101 <223> OTHER INFORMATION: same
W--> 104 <400> 6
105 gacctcctga tcagggatac 20
108 <210> SEQ ID NO: 7
109 <211> LENGTH: 24
110 <212> TYPE: DNA
111 <213> ORGANISM: Artificial
113 <220> FEATURE:
114 <221> NAME/KEY: primer_bind
115 <222> LOCATION: (1)..(24)
116 <223> OTHER INFORMATION: same
W--> 119 <400> 7
120 gccagaagc ggatagaagg cggg 24
123 <210> SEQ ID NO: 8
124 <211> LENGTH: 24
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial
128 <220> FEATURE:
129 <221> NAME/KEY: primer_bind
130 <222> LOCATION: (1)..(24)
131 <223> OTHER INFORMATION: same
W--> 134 <400> 8
135 ctgtggttca gggctcagtc cttc 24
138 <210> SEQ ID NO: 9
139 <211> LENGTH: 24
140 <212> TYPE: DNA

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/550,498

DATE: 10/05/2005

TIME: 16:19:28

Input Set : A:\persico.ST25.txt

Output Set: N:\CRF4\10052005\J550498.raw

```

141 <213> ORGANISM: Artificial
143 <220> FEATURE:
144 <221> NAME/KEY: primer_bind
145 <222> LOCATION: (1)..(24)
146 <223> OTHER INFORMATION: same
W--> 149 <400> 9
150 ggaagagtga gcggcgcatc aagg 24
153 <210> SEQ ID NO: 10
154 <211> LENGTH: 22
155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial
158 <220> FEATURE:
159 <221> NAME/KEY: primer_bind
160 <222> LOCATION: (1)..(22)
161 <223> OTHER INFORMATION: same
W--> 164 <400> 10
165 ctgctggaga ggattattcct cg 22
168 <210> SEQ ID NO: 11
169 <211> LENGTH: 25
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial
173 <220> FEATURE:
174 <221> NAME/KEY: primer_bind
175 <222> LOCATION: (1)..(25)
176 <223> OTHER INFORMATION: same
W--> 179 <400> 11
180 cctgctggat tacattaaag cactg 25
183 <210> SEQ ID NO: 12
184 <211> LENGTH: 25
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial
188 <220> FEATURE:
189 <221> NAME/KEY: primer_bind
190 <222> LOCATION: (1)..(25)
191 <223> OTHER INFORMATION: same
W--> 194 <400> 12
195 cctgaagtac tcattatagt caagg 25
198 <210> SEQ ID NO: 13
199 <211> LENGTH: 27
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial
203 <220> FEATURE:
204 <221> NAME/KEY: primer_bind
205 <222> LOCATION: (1)..(27)
206 <223> OTHER INFORMATION: same
W--> 209 <400> 13
210 gtaagtcgct tattaact tgcgtgc 27
213 <210> SEQ ID NO: 14
214 <211> LENGTH: 27

```

## RAW SEQUENCE LISTING

DATE: 10/05/2005

PATENT APPLICATION: US/10/550,498

TIME: 16:19:28

Input Set : A:\persico.ST25.txt

Output Set: N:\CRF4\10052005\J550498.raw

```

215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial
218 <220> FEATURE:
219 <221> NAME/KEY: primer_bind
220 <222> LOCATION: (1)..(27)
221 <223> OTHER INFORMATION: same
W--> 224 <400> 14
225 gacagcaagt tttaataagc gacttac 27
228 <210> SEQ ID NO: 15
229 <211> LENGTH: 38
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial
233 <220> FEATURE:
234 <221> NAME/KEY: primer_bind
235 <222> LOCATION: (1)..(38)
236 <223> OTHER INFORMATION: same
W--> 239 <400> 15
240 cttgctgtct gaatggaaac acttgcattc tgggggtcc 38
243 <210> SEQ ID NO: 16
244 <211> LENGTH: 38
245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial
248 <220> FEATURE:
249 <221> NAME/KEY: primer_bind
250 <222> LOCATION: (1)..(38)
251 <223> OTHER INFORMATION: same
W--> 254 <400> 16
255 ggacccccagg atgcaagtgt ttccattcag acagcaag 38
258 <210> SEQ ID NO: 17
259 <211> LENGTH: 23
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial
263 <220> FEATURE:
264 <221> NAME/KEY: primer_bind
265 <222> LOCATION: (1)..(23)
266 <223> OTHER INFORMATION: same
W--> 269 <400> 17
270 gaatggaggg gcttgcattc tgg 23
273 <210> SEQ ID NO: 18
274 <211> LENGTH: 23
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial
278 <220> FEATURE:
279 <221> NAME/KEY: primer_bind
280 <222> LOCATION: (1)..(23)
281 <223> OTHER INFORMATION: same
W--> 284 <400> 18
285 ccaggatgca agccccctcca ttc 23
288 <210> SEQ ID NO: 19

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/550,498

DATE: 10/05/2005

TIME: 16:19:28

Input Set : A:\persico.ST25.txt

Output Set: N:\CRF4\10052005\J550498.raw

```

289 <211> LENGTH: 29
290 <212> TYPE: DNA
291 <213> ORGANISM: Artificial
293 <220> FEATURE:
294 <221> NAME/KEY: primer_bind
295 <222> LOCATION: (1)..(29)
296 <223> OTHER INFORMATION: same
W--> 299 <400> 19
300 cttgcatcct gggggccttc tgtgcctgc 29
303 <210> SEQ ID NO: 20
304 <211> LENGTH: 29
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial
308 <220> FEATURE:
309 <221> NAME/KEY: primer_bind
310 <222> LOCATION: (1)..(29)
311 <223> OTHER INFORMATION: same
W--> 314 <400> 20
315 gcaggcacag aaggcccca ggatgcaag 29
318 <210> SEQ ID NO: 21
319 <211> LENGTH: 31
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial
323 <220> FEATURE:
324 <221> NAME/KEY: primer_bind
325 <222> LOCATION: (1)..(31)
326 <223> OTHER INFORMATION: same
W--> 329 <400> 21
330 gcatcctggg gtccgcctgt gcctgccctc c 31
333 <210> SEQ ID NO: 22
334 <211> LENGTH: 31
335 <212> TYPE: DNA
336 <213> ORGANISM: Artificial
338 <220> FEATURE:
339 <221> NAME/KEY: primer_bind
340 <222> LOCATION: (1)..(31)
341 <223> OTHER INFORMATION: same
W--> 344 <400> 22
345 gcatcctggg gtccgcctgt gcctgccctc c 31
348 <210> SEQ ID NO: 23
349 <211> LENGTH: 31
350 <212> TYPE: DNA
351 <213> ORGANISM: Artificial
353 <220> FEATURE:
354 <221> NAME/KEY: primer_bind
355 <222> LOCATION: (1)..(31)
356 <223> OTHER INFORMATION: same
W--> 359 <400> 23
360 gcatcctggg gtccgcctgt gcctgccctc c

```

*FYI (globalenv)*

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/550,498

DATE: 10/05/2005  
TIME: 16:19:29

Input Set : A:\persico.ST25.txt  
Output Set: N:\CRF4\10052005\J550498.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27

Seq#:28,29,30,31,32,33,34,35,36,37,38,39,40,41,42



## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/550,498

DATE: 10/05/2005

TIME: 16:19:29

Input Set : A:\persico.ST25.txt

Output Set: N:\CRF4\10052005\J550498.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:29 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:26  
L:44 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:41  
L:59 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:56  
L:74 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:71  
L:89 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:86  
L:104 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:101  
L:119 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:116  
L:134 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:131  
L:149 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:146  
L:164 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:161  
L:179 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:176  
L:194 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:191  
L:209 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:206  
L:224 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:221  
L:239 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:236  
L:254 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:251  
L:269 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:266  
L:284 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18,Line#:281  
L:299 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:296  
L:314 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:311  
L:329 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:326  
L:344 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:341  
L:359 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:356  
L:374 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24,Line#:371  
L:389 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:386  
L:404 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:401  
L:419 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:416  
L:434 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:28,Line#:431  
L:449 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:446  
L:464 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:30,Line#:461  
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L:494 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32,Line#:491  
L:509 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:33,Line#:506  
L:566 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:34,Line#:563  
L:619 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:35,Line#:616  
L:676 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:36,Line#:673  
L:725 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:37,Line#:722  
L:774 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:38,Line#:771  
L:807 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:39,Line#:804  
L:844 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:40,Line#:841  
L:905 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:41,Line#:902  
L:962 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:42,Line#:959

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